



sequence listing 09-237,981.ST25  
SEQUENCE LISTING

<110> Quertermous, Thomas  
Hogan, Brigid  
Snodgrass, Ralph H  
Zupancic, Thomas J

<120> Antibodies Binding to Polypeptides Encoded by  
Developmentally-Regulated Endothelial Cell Locus-1

<130> 213-0094US

<140> US 09/237,981

<141> 1999-01-25

<150> US 08/659,235

<151> 1996-06-05

<150> US 08/480,229

<151> 1995-06-07

<160> 33

<170> PatentIn version 3.2

<210> 1

<211> 81

<212> PRT

<213> Mus sp.

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1 5 10 15

Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu Ala Tyr  
20 25 30

Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg  
35 40 45

Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys  
50 55 60

Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro  
65 70 75 80

Leu

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<211> 81

<212> PRT

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<213> Homo sapiens

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Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala  
1 5 10 15

Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr  
20 25 30

Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg Thr Gly  
35 40 45

Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys  
50 55 60

Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro  
65 70 75 80

Val

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Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile His Tyr  
20 25 30

Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser Ser Met  
35 40 45

Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val Lys  
50 55 60

Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val Ile Pro  
65 70 75 80

Lys

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Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Val  
 1 5 10 15

Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile Ser Ser  
 20 25 30

Ser Gln Asp Gly His His Trp Thr Gln Ile Leu Tyr Asn Gly Lys Val  
 35 40 45

Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro Met Met Asn Ser  
 50 55 60

Leu Asp Pro Pro Leu Leu Thr Arg  
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Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala  
 1 5 10 15

Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val  
 20 25 30

Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Thr Leu Lys Asp Gly Asn  
 35 40 45

Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val Val Tyr  
 50 55 60

Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu Arg Pro  
 65 70 75 80

Val Thr Trp

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Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Gly  
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Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile Gly Tyr  
 20 25 30

Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser Lys Asn  
 35 40 45

Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro Glu Leu  
 50 55 60

Arg Thr Phe Ala His Ile Thr Thr Gly Phe Ile Arg Ile Ile Pro  
 65 70 75

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Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Arg  
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Gly Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile Arg Tyr Ser Leu  
 20 25 30

Asp Asn Val Ser Trp Phe Glu Tyr Arg Asn Gly Ala Ala Ile Thr Gly  
 35 40 45

Val Thr Asp Arg Asn Thr Val Val Asn His Phe Phe Asp Thr Pro Ile  
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Arg Ala Arg Ser Ile Ala Ile His Pro Leu Thr  
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Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile  
 20 25 30

Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35 40 45

Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa  
 50 55 60

Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa  
 65 70 75 80

Xaa Pro Xaa Xaa Xaa  
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cctgctgtctc atatttctgc atgctgcttt gtttgtatat agtgcgctcc tggcctcagg 180

ctcgtctccc tccagctctc gcttcattgt tctccaagtc agaagcccc gcacccgccc 240

cgcagcagcg tgagccgtag tcaactgctgg ccgcttcgcc tgcgtgcgcg cacggaaatc 300

ggggagccag gaacccaagg agccgcccgtc cgcgcgctgt gcctctgcta gaccactcgc 360

agccccagcc tctctcaagc gcacccacct ccgcgcaccc cagctcaggc gaagctggag 420

tgaggggtgaa tcaccctttc tctagggcca ccactctttt atcgcccttc ccaagatttg 480

agaagcgctg cgggaggaaa gacgtcctct tgatctctga cagggcgggg tttactgctg 540

tcctgcaggc gcgcctcgcc tactgtgccc tccgctacga ccccggaacca gcccagggtca 600

cgtccgtgag aagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt 651

Met Lys His Leu Val Ala Ala Trp Leu Leu Val  
1 5 10

gga ctc agc ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac 699

Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn  
15 20 25

ccg aac ccc tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat 747

Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp  
30 35 40

gat tcc ttt tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc 795

Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys  
45 50 55

tct agt gtt gtg gag gtt gca tca gat gaa gaa aag cct act tca gca 843

Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala  
60 65 70 75

ggg ccc tgc atc cct aac cca tgc cat aac gga gga acc tgt gag ata 891

Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile  
80 85 90

agc gaa gcc tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt 939

Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys  
95 100 105

cct cgg gga ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt 987

Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys  
110 115 120

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gaa gct gag cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct Glu Ala Glu Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala 125 130 135	1035
aac tac tct tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln 140 145 150 155	1083
tat aaa tgc tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat Tyr Lys Cys Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn 160 165 170	1131
cag caa atc aca gct tca tct aat cac cga gct ctt ttt gga ctc cag Gln Gln Ile Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln 175 180 185	1179
aag tgg tat ccc tac tat gct cga ctt aat aag aag ggc ctt ata aat Lys Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn 190 195 200	1227
gcc tgg aca gct gct gaa aat gac aga tgg cca tgg att cag ata aat Ala Trp Thr Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn 205 210 215	1275
ttg caa aga aaa atg aga gtc act ggt gtt att acc caa gga gca aaa Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys 220 225 230 235	1323
agg att gga agc cca gag tac ata aaa tcc tac aaa att gcc tac agc Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser 240 245 250	1371
aat gac ggg aag acc tgg gca atg tac aaa gta aaa ggc acc aat gaa Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu 255 260 265	1419
gag atg gtc ttt cgt gga aat gtt gat aac aac aca cca tat gct aat Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn 270 275 280	1467
tct ttc aca ccc cca atc aaa gct cag tat gta aga ctc tac ccc caa Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln 285 290 295	1515
att tgt cga agg cat tgt act tta aga atg gaa ctt ctt ggc tgt gag Ile Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu 300 305 310 315	1563
ctc tca ggc tgt tca gaa cct ttg ggg atg aaa tca ggg cat ata caa Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln 320 325 330	1611
gac tac cag atc act gcc tcc agc gtc ttc aga aca ctc aac atg gac Asp Tyr Gln Ile Thr Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp 335 340 345	1659
atg ttt act tgg gaa cca agg aaa gcc agg ctg gac aag caa ggc aaa Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys 350 355 360	1707



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gta aat gcc tgg act tcc ggc cat aac gac cag tca caa tgg tta cag	1755
Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln	
365 370 375	
ggt gat ctt ctt gtc cct act aag gtg aca ggc atc att aca caa gga	1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly	
380 385 390 395	
gct aaa gat ttt ggt cac gtg cag ttt gtt ggg tca tac aaa cta gct	1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala	
400 405 410	
tac agc aat gat gga gaa cac tgg atg gtg cac cag gat gaa aaa cag	1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln	
415 420 425	
agg aaa gac aag gtt ttt caa ggc aat ttt gac aat gac act cac agg	1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg	
430 435 440	
aaa aat gtc atc gac cct ccc atc tat gca cga ttc ata aga atc ctt	1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu	
445 450 455	
cct tgg tcc tgg tat gga agg atc act ctg cgg tca gag ctg ctg ggc	2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly	
460 465 470 475	
tgc gca gag gag gaa tgaagtgcgg ggccgcacat cccacaatgc ttttctttat	2098
Cys Ala Glu Glu Glu	
480	
tttcctataa gtatctccac gaaatgaact gtgtgaagct gatggaaact gcatttgttt	2158
ttttcaaagt gttcaaatta tggtaggcta ctgactgtct ttttaggagt tctaagcttg	2218
cctttttaat aatttaattt ggtttccttt gctcaactct cttatgtaat atcacactgt	2278
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Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu	
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Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys	
35 40 45	

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Glu 50	Cys	Pro	Glu	Gly	Phe 55	Ala	Gly	Pro	Asn	Cys	Ser 60	Ser	Val	Val	Glu
Val 65	Ala	Ser	Asp	Glu	Glu 70	Lys	Pro	Thr	Ser	Ala 75	Gly	Pro	Cys	Ile	Pro 80
Asn	Pro	Cys	His	Asn 85	Gly	Gly	Thr	Cys	Glu 90	Ile	Ser	Glu	Ala	Tyr 95	Arg
Gly	Asp	Thr	Phe 100	Ile	Gly	Tyr	Val	Cys 105	Lys	Cys	Pro	Arg	Gly 110	Phe	Asn
Gly	Ile	His 115	Cys	Gln	His	Asn 120	Ile	Asn	Glu	Cys	Glu	Ala 125	Glu	Pro	Cys
Arg	Asn 130	Gly	Gly	Ile	Cys	Thr 135	Asp	Leu	Val	Ala	Asn 140	Tyr	Ser	Cys	Glu
Cys 145	Pro	Gly	Glu	Phe 150	Met	Gly	Arg	Asn	Cys	Gln 155	Tyr	Lys	Cys	Ser	Gly 160
His	Leu	Gly	Ile	Glu 165	Gly	Gly	Ile	Ile	Ser 170	Asn	Gln	Gln	Ile	Thr 175	Ala
Ser	Ser	Asn 180	His	Arg	Ala	Leu	Phe	Gly 185	Leu	Gln	Lys	Trp	Tyr 190	Pro	Tyr
Tyr	Ala	Arg 195	Leu	Asn	Lys	Lys	Gly 200	Leu	Ile	Asn	Ala	Trp 205	Thr	Ala	Ala
Glu	Asn 210	Asp	Arg	Trp	Pro	Trp 215	Ile	Gln	Ile	Asn	Leu 220	Gln	Arg	Lys	Met
Arg 225	Val	Thr	Gly	Val	Ile 230	Thr	Gln	Gly	Ala	Lys 235	Arg	Ile	Gly	Ser	Pro 240
Glu	Tyr	Ile	Lys	Ser 245	Tyr	Lys	Ile	Ala	Tyr 250	Ser	Asn	Asp	Gly	Lys 255	Thr
Trp	Ala	Met	Tyr 260	Lys	Val	Lys	Gly	Thr 265	Asn	Glu	Glu	Met	Val 270	Phe	Arg
Gly	Asn	Val	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro	Pro

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275

280

285

Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His  
290 295 300

Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser  
305 310 315 320

Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr  
325 330 335

Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu  
340 345 350

Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr  
355 360 365

Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val  
370 375 380

Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly  
385 390 395 400

His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly  
405 410 415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val  
420 425 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp  
435 440 445

Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr  
450 455 460

Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu  
465 470 475 480

<210> 11

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cgc tga gga aag aga acg tct tct tga att ctt tag tag ggg cgg agt	96
Arg Gly Lys Arg Thr Ser Ser Ile Leu Gly Arg Ser	
20 25	
ctg ctg ctg ccc tgc gct gcc acc tcg gct aca ctg ccc tcc gcg acg	144
Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro Ser Ala Thr	
30 35 40	
acc cct gac cag ccg ggg tca cgt ccg gga gac ggg atc atg aag cgc	192
Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile Met Lys Arg	
45 50 55	
tcg gta gcc gtc tgg ctc ttg gtc ggg ctc agc ctc ggt gtc ccc cag	240
Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly Val Pro Gln	
60 65 70 75	
ttc ggc aaa ggt gat att tgt gat ccc aat cca tgt gaa aat gga ggt	288
Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly	
80 85 90	
atc tgt ttg cca gga ttg gct gta ggt tcc ttt tcc tgt gag tgt cca	336
Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro	
95 100 105	
gat ggc ttc aca gac ccc aac tgt tct agt gtt gtg gag gtt gca tca	384
Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser	
110 115 120	
gat gaa gaa gaa cca act tca gca ggt ccc tgc act cct aat cca tgc	432
Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro Asn Pro Cys	
125 130 135	
cat aat gga gga acc tgt gaa ata agt gaa gca tac cga ggg gat aca	480
His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg Gly Asp Thr	
140 145 150 155	
ttc ata ggc tat gtt tgt aaa tgt ccc cga gga ttt aat ggg att cac	528
Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn Gly Ile His	
160 165 170	
tgt cag cac aac ata aat gaa tgc gaa gtt gag cct tgc aaa aat ggt	576
Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys Lys Asn Gly	
175 180 185	
gga ata tgt aca gat ctt gtt gct aac tat tcc tgt gag tgc cca ggc	624
Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu Cys Pro Gly	
190 195 200	
gaa ttt atg gga aga aat tgt caa tac aaa tgc tca ggc cca ctg gga	672
Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly Pro Leu Gly	
205 210 215	

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att gaa ggt gga att ata tca aac cag caa atc aca gct tcc tct act	720
Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala Ser Ser Thr	
220 225 230 235	
cac cga gct ctt ttt gga ctc caa aaa tgg tat ccc tac tat gca cgt	768
His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr Tyr Ala Arg	
240 245 250	
ctt aat aag aag ggg ctt ata aat gcg tgg aca gct gca gaa aat gac	816
Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala Glu Asn Asp	
255 260 265	
aga tgg aac cgg tgg att cag ata aat ttg caa aga aaa atg aga gtt	864
Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys Met Arg Val	
270 275 280	
act ggt gtg att acc caa ggg gcc aag agg att gga agc cca gag tat	912
Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro Glu Tyr	
285 290 295	
ata aaa ttc tac aaa att gcc tac agt aat gat gga aag act tgg gca	960
Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr Trp Ala	
300 305 310 315	
atg tac aaa gtg aaa ggc acc aat gaa gac atg gtg ttt cgt gga aac	1008
Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe Arg Gly Asn	
320 325 330	
att gat aac aac act cca tat gct aac tct ttc aca ccc ccc ata aaa	1056
Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro Ile Lys	
335 340 345	
gct cag tat gta aga ctc tat ccc caa gtt tgt cga aga cat tgc act	1104
Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg His Cys Thr	
350 355 360	
ttg cga atg gaa ctt ctt ggc tgt gaa ctg tcg ggt tgt tct gag cct	1152
Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser Glu Pro	
365 370 375	
ctg ggt atg aaa tca gga cat ata caa gac tat cag atc act gcc tcc	1200
Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr Ala Ser	
380 385 390 395	
agc atc ttc aga acg ctc aac atg gac atg ttc act tgg gaa cca agg	1248
Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu Pro Arg	
400 405 410	
aaa gct cgg ctg gac aag caa ggc aaa gtg aat gcc tgg acc tct ggc	1296
Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr Ser Gly	
415 420 425	
cac aat gac cag tca caa tgg tta cag gtg gat ctt ctt gtt cca acc	1344
His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val Pro Thr	
430 435 440	
aaa gtg act ggc atc att aca caa gga gct aaa gat ttt ggt cat gta	1392
Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly His Val	
445 450 455	

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cag ttt gtt ggc tcc tac aaa ctg gct tac agc aat gat gga gaa cac	1440
Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly Glu His	
460 465 470 475	
tgg act gta tac cag gat gaa aag caa aga aaa gat aag gtt ttc cag	1488
Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val Phe Gln	
480 485 490	
gga aat ttt gac aat gac act cac aga aaa aat gtc atc gac cct ccc	1536
Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp Pro Pro	
495 500 505	
atc tat gca cga cac ata aga atc ctt cct tgg tcc tgg tac ggg agg	1584
Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr Gly Arg	
510 515 520	
atc aca ttg gcg tca gag ctg ctg ggc tgc aca gag gag gaa tga ggg	1632
Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu Gly	
525 530 535	
gag gct aca ttt cac aac cgt ctt ccc tat ttg ggt aaa agt atc tcc	1680
Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile Ser	
540 545 550	
atg gaa tga act gtg taa aat ctg tag gaa act gaa tgg ttt ttt ttt	1728
Met Glu Thr Val Asn Leu Glu Thr Glu Trp Phe Phe Phe	
555 560 565	
ttt tca tga aaa agt ggt caa att atg gta ggc aac taa cgg tgt ttt	1776
Phe Ser Lys Ser Gly Gln Ile Met Val Gly Asn Arg Cys Phe	
570 575 580	
tac c	1780
Tyr	

<210> 12  
 <211> 14  
 <212> PRT  
 <213> homo sapiens

<400> 12

Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys Arg
1 5 10

<210> 13  
 <211> 6  
 <212> PRT  
 <213> homo sapiens

<400> 13

Gly Lys Arg Thr Ser Ser
1 5

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<210> 14  
 <211> 513  
 <212> PRT  
 <213> homo sapiens

<400> 14

Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro  
 1 5 10 15

Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile  
 20 25 30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly  
 35 40 45

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu  
 50 55 60

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys  
 65 70 75 80

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu  
 85 90 95

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro  
 100 105 110

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg  
 115 120 125

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn  
 130 135 140

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys  
 145 150 155 160

Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu  
 165 170 175

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly  
 180 185 190

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala  
 195 200 205

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Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr	210	215	220
Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala	225	230	235
Glu	Asn	Asp	Arg	Trp	Asn	Arg	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys	245	250	255
Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	Ile	Gly	Ser	260	265	270
Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys	275	280	285
Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	Met	Val	Phe	290	295	300
Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro	305	310	315
Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val	Cys	Arg	Arg	325	330	335
His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	Ser	Gly	Cys	340	345	350
Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	Tyr	Gln	Ile	355	360	365
Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	Phe	Thr	Trp	370	375	380
Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val	Asn	Ala	Trp	385	390	395
Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val	Asp	Leu	Leu	405	410	415
Val	Pro	Thr	Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Lys	Asp	Phe	420	425	430
Gly	His	Val	Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	Tyr	Ser	Asn	Asp	435	440	445



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Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys  
450 455 460

Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile  
465 470 475 480

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp  
485 490 495

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu  
500 505 510

Glu

<210> 15  
<211> 19  
<212> PRT  
<213> homo sapiens

<400> 15

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile  
1 5 10 15

Ser Met Glu

<210> 16  
<211> 9  
<212> PRT  
<213> homo sapiens

<400> 16

Glu Thr Glu Trp Phe Phe Phe Phe Ser  
1 5

<210> 17  
<211> 9  
<212> PRT  
<213> homo sapiens

<400> 17

Lys Ser Gly Gln Ile Met Val Gly Asn  
1 5

sequence listing 09-237,981.ST25

<210> 18  
 <211> 4  
 <212> PRT  
 <213> homo sapiens

<400> 18

Arg Cys Phe Tyr  
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 <213> mus sp.

<400> 19  
 gacagatggc catggattca gataaatttg caaagaaaaa tgagagtcac tgggtgttatt 60  
 acccaaggag caaaaaggat tggaagccca gagtacataa aatcctacaa aattgcctac 120  
 agcaatgacg ggaagacctg ggcaatgtac aaagtaaaag gcaccaatga agagatggtc 180  
 tttcgtggaa atgttgataa caacacacca tatgctaatt ctttcacacc cccaatcaaa 240  
 gctcagtatg taagactcta cccccaaatt tgtcgaaggc attgtacttt aagaatggaa 300  
 cttcttggct gtgagctc 318

<210> 20  
 <211> 316  
 <212> PRT  
 <213> homo sapiens

<400> 20

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln  
 1 5 10 15

Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp  
 20 25 30

Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp  
 35 40 45

His Ala Ser Asn Tyr Asp Ser Lys Pro Trp Ile Gln Val Asn Leu Leu  
 50 55 60

Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg Ala  
 65 70 75 80

Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu Asp  
 85 90 95

sequence listing 09-237,981.ST25

Gly	Arg	Lys	Phe	Glu	Phe	Ile	Gln	Asp	Glu	Ser	Gly	Gly	Asp	Lys	Glu	100	105	110
Phe	Leu	Gly	Asn	Leu	Asp	Asn	Asn	Ser	Leu	Lys	Val	Asn	Met	Phe	Asn	115	120	125
Pro	Thr	Leu	Glu	Ala	Gln	Tyr	Ile	Arg	Leu	Tyr	Pro	Val	Ser	Cys	His	130	135	140
Arg	Gly	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu	Leu	His	Gly	145	150	155
Cys	Leu	Glu	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Thr	Ile	Pro	Asp	Ser	Gln	165	170	175
Met	Ser	Ala	Ser	Ser	Ser	Tyr	Lys	Thr	Trp	Asn	Leu	Arg	Ala	Phe	Gly	180	185	190
Trp	Tyr	Pro	His	Leu	Gly	Arg	Leu	Asp	Asn	Gln	Gly	Lys	Ile	Asn	Ala	195	200	205
Trp	Thr	Ala	Gln	Ser	Asn	Ser	Ala	Lys	Glu	Trp	Leu	Gln	Val	Asp	Leu	210	215	220
Gly	Thr	Gln	Arg	Gln	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Arg	Asp	225	230	235
Phe	Gly	His	Ile	Gln	Tyr	Val	Glu	Ser	Tyr	Lys	Val	Ala	His	Ser	Asp	245	250	255
Asp	Gly	Val	Gln	Trp	Thr	Val	Tyr	Glu	Glu	Gln	Gly	Ser	Ser	Lys	Val	260	265	270
Phe	Gln	Gly	Asn	Leu	Asp	Asn	Asn	Ser	His	Lys	Lys	Asn	Ile	Phe	Glu	275	280	285
Lys	Pro	Phe	Met	Ala	Arg	Tyr	Val	Arg	Val	Leu	Pro	Val	Ser	Trp	His	290	295	300
Asn	Arg	Ile	Thr	Leu	Arg	Leu	Glu	Leu	Leu	Gly	Cys					305	310	315

<210> 21

sequence listing 09-237,981.ST25

<211> 321  
 <212> PRT  
 <213> homo sapiens

<220>  
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 <222> (225)..(225)

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 <222> (225)..(225)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
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 <222> (243)..(243)

<220>  
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 <222> (243)..(243)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
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<220>  
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 <222> (266)..(266)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
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<220>  
 <221> misc\_feature  
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 <223> Xaa can be any naturally occurring amino acid

<400> 21

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln  
 1 5 10 15

Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp  
 20 25 30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp  
 35 40 45

Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu  
 50 55 60

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Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	65	70	75	80
Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	85	90	95	
Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	100	105	110	
Met	Val	Phe	Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	115	120	125	
Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val	130	135	140	
Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	145	150	155	160
Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	165	170	175	
Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	180	185	190	
Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val	195	200	205	
Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val	210	215	220	
Xaa	Leu	Leu	Val	Pro	Thr	Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	225	230	235	240
Lys	Asp	Xaa	Gly	His	Val	Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	Tyr	245	250	255	
Ser	Asn	Asp	Gly	Glu	His	Trp	Thr	Val	Xaa	Gln	Asp	Glu	Lys	Gln	Arg	260	265	270	
Lys	Asp	Lys	Val	Xaa	Gln	Gly	Asn	Phe	Asp	Asn	Asp	Thr	His	Arg	Lys	275	280	285	
Asn	Val	Ile	Asp	Pro	Pro	Ile	Tyr	Ala	Arg	His	Ile	Arg	Ile	Leu	Pro	290	295	300	

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Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys  
305 310 315 320

Thr

<210> 22  
<211> 25  
<212> PRT  
<213> homo sapiens

<400> 22

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly  
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile  
20 25

<210> 23  
<211> 52  
<212> PRT  
<213> homo sapiens

<400> 23

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu  
1 5 10 15

Ala Val Gly Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro  
20 25 30

Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Glu Pro Thr  
35 40 45

Ser Ala Gly Pro  
50

<210> 24  
<211> 45  
<212> PRT  
<213> homo sapiens

<400> 24

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu  
1 5 10 15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg

sequence listing 09-237,981.ST25

20

25

30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu  
35 40 45

<210> 25

<211> 35

<212> PRT

<213> homo sapiens

<400> 25

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val  
1 5 10 15

Ala Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys  
20 25 30

Gln Tyr Lys  
35

<210> 26

<211> 40

<212> PRT

<213> artificial sequence

<220>

<223> Consensus EGF domain

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<222> (2)..(4)

<223> nonconsensus sequence

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<222> (7)..(7)

<223> nonconsensus sequence

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<222> (11)..(11)

<223> nonconsensus sequence

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<222> (13)..(25)

<223> nonconsensus sequence

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<222> (26)..(26)

<223> Y or F

sequence listing 09-237,981.ST25

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 <223> nonconsensus sequence

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 <222> (29)..(29)  
 <223> nonconsensus sequence

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 <222> (31)..(32)  
 <223> nonconsensus sequence

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 <222> (34)..(34)  
 <223> Y or F

<220>  
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 <222> (37)..(38)  
 <223> nonconsensus sequence

<220>  
 <221> MISC\_FEATURE  
 <222> (40)..(40)  
 <223> nonconsensus sequence

<400> 26

Cys	Xaa	Xaa	Xaa	Pro	Cys	Xaa	Asn	Gly	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys	Xaa	Xaa
			20					25					30		

Gly	Xaa	Xaa	Gly	Xaa	Xaa	Cys	Xaa
			35				40

<210> 27  
 <211> 310  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(1)



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<223> n is a, c, g, t or u

<400> 27

ngt gat attt	gt gat cccaa	tcc at gtgaa	aat ggaggta	tct gtttgcc	agg attggct	60
gtaggttcct	ttt cctgtga	gtgtccagat	ggcttcacag	accccaactg	ttctagtgtt	120
gtggagggttg	gtccctgcac	tcctaatacca	tgccataatg	gaggaacctg	tgaaataagt	180
gaagcataacc	gaggggatac	attcataggc	tatgtttgta	aatgtcccg	aggatttaat	240
gggattcact	gtcagcacia	cataaatgaa	tgcaagttg	agccttgcaa	aaatggtgga	300
atatgtacag						310

<210> 28

<211> 2308

<212> DNA

<213> mus sp.

<220>

<221> CDS

<222> (550)..(1212)

<220>

<221> misc\_feature

<222> (1819)..(1821)

<223> n is a, c, g, t or u

<400> 28

gaattccggg	agggagggtg	ggggggcggg	ccgcgggggc	ccaaagccag	ctaggctcag	60
tctcacacgc	gcgccgccac	tgtttgtata	tagtgcgctc	ctggcctcag	gctcgctccc	120
ctccagctct	cgcttcattg	ttctccaagt	cagaagcccc	cgcatccgcc	gcgcagcagc	180
gtgagccgta	gtcactgctg	gccgcttcgc	ctgcgtgcgc	gcacggaaat	cggggagcca	240
ggaacccaag	gagccgccgt	ccgcccgtg	tgcctctgct	agaccactcg	cagccccagc	300
ctctctcaag	cgcacccacc	tccgcgccac	ccagctcagg	cgaagctgga	gtgagggtga	360
atcacccttt	ctctagggcc	accactcttt	tatcgccctt	cccaagattt	gagaagcgct	420
gcgggaggaa	agacgtctct	ttgatctctg	acagggcggg	gtttactgct	gtcctgcagg	480
cgcgctcgc	ctactgtgcc	ctccgctacg	accccgacc	agcccaggtc	acgtccgtga	540
gaagggatc	atg aag cac	ttg gta gca	gcc tgg ctt	ttg gtt gga	ctc agc	591
	Met Lys His	Leu Val Ala	Ala Trp Leu	Leu Val Gly	Leu Ser	
	1	5	10			
ctc ggg gtg	ccc cag ttc	ggc aaa ggt	gac att tgc	aac ccg aac	ccc	639
Leu Gly Val	Pro Gln Phe	Gly Lys Gly	Asp Ile Cys	Asn Pro Asn	Pro	
15	20	25	30			
tgt gaa aat	ggt ggc atc	tgt ctg tca	gga ctg gct	gat gat tcc	ttt	687

sequence listing 09-237,981.ST25

Cys	Glu	Asn	Gly	Gly	Ile	Cys	Leu	Ser	Gly	Leu	Ala	Asp	Asp	Ser	Phe	
				35					40					45		
tcc	tgt	gag	tgt	cca	gaa	ggc	ttc	gca	ggg	ccg	aac	tgc	tct	agt	gtt	735
Ser	Cys	Glu	Cys	Pro	Glu	Gly	Phe	Ala	Gly	Pro	Asn	Cys	Ser	Ser	Val	
			50				55					60				
gtg	gag	gtt	gca	tca	gat	gaa	gaa	aag	cct	act	tca	gca	ggg	ccc	tgc	783
Val	Glu	Val	Ala	Ser	Asp	Glu	Glu	Lys	Pro	Thr	Ser	Ala	Gly	Pro	Cys	
		65					70					75				
atc	cct	aac	cca	tgc	cat	aac	gga	gga	acc	tgt	gag	ata	agc	gaa	gcc	831
Ile	Pro	Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	
	80					85					90					
tat	cga	gga	gac	aca	ttc	ata	ggc	tat	gtt	tgt	aaa	tgt	cct	cgg	gga	879
Tyr	Arg	Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	
95					100				105						110	
ttt	aat	ggg	att	cac	tgt	cag	cac	aat	ata	aat	gaa	tgt	gaa	gct	gag	927
Phe	Asn	Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Ala	Glu	
				115					120					125		
cct	tgc	aga	aat	ggc	gga	ata	tgt	acc	gac	ctt	gtt	gct	aac	tac	tct	975
Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	
			130					135					140			
tgt	gaa	tgc	cca	gga	gaa	ttt	atg	gga	cga	aat	tgt	caa	tat	aaa	tgc	1023
Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	
		145					150					155				
tct	ggg	cac	ttg	gga	atc	gaa	ggg	ggg	atc	ata	tct	aat	cag	caa	atc	1071
Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	
	160					165					170					
aca	gct	tca	tct	aat	cac	cga	gct	ctt	ttt	gga	ctc	cag	aag	tgg	tat	1119
Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	
175					180				185						190	
ccc	tac	tat	gct	aga	ctt	aat	aag	aag	ggc	ctt	ata	aat	gcc	tgg	aca	1167
Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	
				195					200				205			
gct	gct	gaa	aat	gac	aga	tgg	cca	tgg	att	cag	gta	aca	gtg	gga		1212
Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Val	Thr	Val	Gly		
		210						215					220			
tgagacaaat	ccatttccca	aattatcaga	atcattatag	aagtaggtta	gggagaattg											1272
gctgtgattc	tttctcatgg	ttaaaatgtg	atttagttca	gaattaacat	ggttggaac											1332
tctaaaaaat	gtggaaaaca	ggaacattct	atgtctgaaa	atctgaaaat	agcatcaaga											1392
tgaaaacatt	ctttagtcac	aaatatactc	ttttaagtta	tagtagagaa	aaagatctta											1452
tcatttcata	agtggacttt	tgggatagca	ttggaaatgt	aaatgaaata	aatacctaata											1512
tgaaaaaagt	ttattctaaa	gtgttaatat	ttagcaacag	attcagagac	aagaaagtaa											1572

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caattcaatc tgtgtatntt ttgtgagaaa tagtttccca tgtgcaaata taaagtgcgc 1632  
atcatatcat gataatatcc aactgtctgc agaactccct ttcataaatg agagaatntt 1692  
aattcatagt gccttatatc ctcatcagcc atctgactnt actacagaag aaaacaatga 1752  
aatgatgcat taagtgcntt gctagaagaa acatcatagc aaagctgata gccacattc 1812  
tgtgcannna agcttcaga gcactcgaga aaaagcagaa atgagatgnt ttatgaaaac 1872  
cgaaaagata atctgatttc tgtgaaatat actnttgatc atgtgnttct ttaagatagt 1932  
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aaggatacct tcaactggcc tagattntca agaaacagtg taatcaacag ccaaacatga 2112  
gaatctagct aacagcattt agaaaaccag aactaagagt gttactggg aattgcattt 2172  
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Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly  
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Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu  
20 25 30

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys  
35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu  
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro  
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg  
85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn

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100                               105                               110
Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
115                               120                               125
Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130                               135                               140
Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145                               150                               155                               160
His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165                               170                               175
Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180                               185                               190
Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
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Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
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Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly  
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Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu  
 20 25 30

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys  
 35 40 45

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Glu	Cys	Pro	Asp	Gly	Phe	Thr	Asp	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu	50	55	60
Val	Ala	Ser	Asp	Glu	Glu	Glu	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Thr	Pro	65	70	75
Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg	85	90	95
Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn	100	105	110
Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Val	Glu	Pro	Cys	115	120	125
Lys	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu	130	135	140
Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly	145	150	155
Pro	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala	165	170	175
Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr	180	185	190
Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala	195	200	205
Glu	Asn	Asp	Arg	Trp	Asn	Arg	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys	210	215	220
Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	Ile	Gly	Ser	225	230	235
Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys	245	250	255
Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	Met	Val	Phe	260	265	270
Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro			

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275

280

285

Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg  
290 295 300

His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys  
305 310 315 320

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile  
325 330 335

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp  
340 345 350

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp  
355 360 365

Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Xaa Leu Leu  
370 375 380

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Xaa  
385 390 395 400

Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp  
405 410 415

Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg Lys Asp Lys  
420 425 430

Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile  
435 440 445

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp  
450 455 460

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu  
465 470 475 480

Glu

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Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe  
 20 25 30

Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Gly Pro Cys Thr Pro  
 35 40 45

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg  
 50 55 60

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn  
 65 70 75 80

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys  
 85 90 95

Lys Asn Gly Gly Ile Cys Thr  
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19

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19



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